

Applicant(s): Bianca A. Thomae et al.  
 PHENYLETHANOLAMINE-N-METHYLTRANSFERASE  
 SEQUENCE VARIANTS

Figure 1 – page 1

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CTGGCACTGGGTGGTAACCAGCAAGCCAGCTGGCATCCGCATCCAGGGTTTGTTCATG
1  -----+-----+-----+-----+-----+-----+ 60
GACCGTGACCCACCATTTGGTCGTTTCGGTCGACCGTAGGCGTAGGTCCCAAACAAAGTTAC

ATGTCTCGTGGAGAATATGGAGGGGCTGGTGCCAGGACTGTCCTTGGCTTTGCCTCGGGG
61  -----+-----+-----+-----+-----+-----+ 120
TACAGAGCACCTCTTATACCTCCCCGACCACGGTCCTGACAGGAACCGAAACGGAGCCCC

TGTGAACGGGGTCAGTGACCTCTAAACTAACCTGCCTCTCAGTTCTGAATCCAGACAGA
121  -----+-----+-----+-----+-----+-----+ 180
ACACTTGCCCCAGTCACTGGAGATTTTGATTGGACGGAGAGTCAAGACTTAGGTCTGTCT

ATCAATCCTCAGCTGTGTCTCGCTCCACACCCCCCTGCCCTGGAAGCCAGGGAAGGTTGGA
181  -----+-----+-----+-----+-----+-----+ 240
TAGTTAGGAGTCGACACAGAGCGAGGTGTGGGGGACGGGACCTTCGGTCCCTTCCAACCT

GGTGCTAGGGGGTCAGGCTCCCCCTCTGTGACCCCTGCAGCTGTTGTGGTGACTCATGTCC
241  -----+-----+-----+-----+-----+-----+ 300
CCACGATCCCCAGTCCGAGGGGAGACACTGGGGACGTCGACAACACCACTGAGTACAGG

CAACCTAGCTGCCTCTCCCAAGGAGACTTTCCCCTGGGACAAGGGGGAGGGAATGGCATG
301  -----+-----+-----+-----+-----+-----+ 360
GTTGGATCGACGGAGAGGGTTCTCTGAAAGGGGACCCTGTTCCCCCTCCCTTACCGTAC

GAGGAGGCCCCACATCAAGCGGGGCCAGGAACCCACGGTGGCAGGAGCTGGGCTGGTGACC
361  -----+-----+-----+-----+-----+-----+ 420
CTCCTCCGGGTGTAGTTTCGCCCCGGTCTTGGGTGCCACCGTCCTCGACCCGACCACTGG

TACCCAGGGCAGAAGGGCCCGGACTCATCCAGAGGGGAAGGAAGGGTCTTCAGGAAGA
421  -----+-----+-----+-----+-----+-----+ 480
ATGGGTCCCGTCTTCCCGGGCCCTGAGTAGGTCTCCCCTTCCTTCCCAGAAGTCCTTCT

CCACGGAGATGCCACAGGCAGAAATTGGCTTCCCATCTGGGAGATAGGTGGGGAGACCCTG
481  -----+-----+-----+-----+-----+-----+ 540
GGTGCCTCTACGGTGTCCGTCTTAACCGAAGGGTAGACCCTCTATCCACCCCTCTGGGAC

GCATTTTGACAGCCAGAACCTGGGGTGCTGAGCAGAATCTTCATGCCTGGCCTGGCCGCC
541  -----+-----+-----+-----+-----+-----+ 600
CGTAAACTGTTCGGTCTTGGACCCACGACTCGTCTTAGAAGTACGGACCGGACCGGCGG

TTCGGAGGGAAGCTGGAGGGTTGGGTGCGAGAGGAGTGGGGTCAGAGCCCCCTACATCCGC
601  -----+-----+-----+-----+-----+-----+ 660
AAGCCTCCCTTCGACCTCCCAACCCACGCTCTCCTCACCCAGTCTCGGGGATGTAGGCG

AGGACCCCAAATCGGCTGGGCCCCAAGGCCCGGACTGCGCTCCCCGGTGGCCCCGGCGGC
661  -----+-----+-----+-----+-----+-----+ 720
TCCTGGGGTTTAGCCGACCGGGGTTCGGGGCTGACGCGAGGGGCCACCGGGGCCGCCG

CCTCCGCGAATGCGTCTGCCCCCTCCCCTGCCCAAGCCCTCTGCCCTCACCCGGGTCCGG
721  -----+-----+-----+-----+-----+-----+ 780
GGAGGCGCTTACGCAGGACGGGGAGGGGACGGGTTCGGGAGACGGGAGTGGGCCAGGCC

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CGCCGCCCCCGAAGTGGCGGGAACAACCCGAACCCGAACCTTCTGTCTCTCGGGAGCCCCC
781 -----+-----+-----+-----+-----+-----+-----+ 840
GCGGCGGGGGCTTCACCGCCCTTGTGTTGGGCTTGGGCTTGGGAAGACAGGAGCCCTCGGGGG

AGATAAGCGCTGGGAACCCGCGGGGCGCAGGGGAGGCCCGGCTGTTCCGCCCCGTAA
841 -----+-----+-----+-----+-----+-----+-----+ 900
TCTATTGCGCGACCTTGGGCGCCCCGGGCGTCCCCTCCGGGCCGACAAGGCGGGCGATT

GTGCATTAGCACAGCTCACCTCCCCATCGCGCCTGCCATCGGACGGGCAGTGCCGCGCC
901 -----+-----+-----+-----+-----+-----+-----+ 960
CACGTAATCGTGTGAGTGGAGGGGATAGCGCGGACGGTAGCCTGCCCCGTCACGGCGCGG

CTGCTCTGGGGCCCCCGGAGCGACCACAGCGGAGGCCGGAACGGACTGTCTTTCTGGGG
961 -----+-----+-----+-----+-----+-----+-----+ 1020
GACGAGACCCCGGGGGCCTCGCTGGTGTGCTCCTCCGGCCTTGCTGACAGGAAAGACCCC

CGGGGTGGGGAGGGGGTGTGCTGGAGGGCCCGGTGGCATAGCAACGGACGAGAGAGGCC
1021 -----+-----+-----+-----+-----+-----+-----+ 1080
GCCCCACCCCTCCCCACAGCGACCTCCCGGGCCACCGTATCGTTGCCTGCTCTCTCCGG

TGGAGGAGGGGCGGGGAGGGGGAGTTGTGTGGCAGTTCTAAGGGAAGGGTGGGTGCTGGG
1081 -----+-----+-----+-----+-----+-----+-----+ 1140
ACCTCCTCCCCGCCCTCCCCCTCAACACACCGTCAAGATTCCCTTCCCACCCACGACCC

ACGGGTGTCCGGGAGGGAGGGGAGCCTGGCGGGGTCTGGGGCCTCGTCGCGGAGGGCGCT
1141 -----+-----+-----+-----+-----+-----+-----+ 1200
TGCCACAGGCCCTCCCTCCCTCGGACCGCCCCAGACCCCGGAGCAGCGCCTCCCGCA

GCGAGGGGGAACTGGGGAAAGGGCCTAATTCCCCAGTCTCCACCTCGAATCAGGAAAGA
1201 -----+-----+-----+-----+-----+-----+-----+ 1260
CGCTCCCCCTTTGACCCCTTTCCCGGATTAAGGGGTGAGAGGTGGAGCTTAGTCCCTTTCT

GAAGGGGCGGGCTGCTGGGCAAAAGAGGTGAATGGCTGCGGGGGCTGGAGAAGAGAGAT
1261 -----+-----+-----+-----+-----+-----+-----+ 1320
CTTCCCCGCGCGACGACCCGTTTCTCACTTACCGACGCCCCCGACCTCTTCTCTCTA

GGGAGGGGCGGCGCGGGGGGTGAGGGGGTCTAAAGATTGTGGGGGTGAGGAACTGAGG
1321 -----+-----+-----+-----+-----+-----+-----+ 1380
CCCTCCCCGCGCGCGCGGGGCTCCCCACTCCCCAGATTCTAACACCCCCACTCCTTGACTCC

GTGGGGGGCGCCCAGAGGCGGGACTCGGGGCGGGGCGAGGCGAGGCGGAGGGGCTG
1381 -----+-----+-----+-----+-----+-----+-----+ 1440
CACCCCCGCGGGTCTCCGCCCTGAGCCCCGCCCCGTCCGCTCCGCTCCCGCTCCCGAC

CGGGAGCAAGTACGAGCCGGGGGTGTGGGGGACGATTGCCGCTGCAGCCGCCGCCAC
1441 -----+-----+-----+-----+-----+-----+-----+ 1500
GCCCTCGTTCATGCCTCGGCCCCACACCCCTGCTAACGGCGACGTCGGCGGCGGGGTG

TCACCTCCGGTGTGTCTGCAGCCCGGACACTAAGGGAGATGGATGAATGGGTGGGGAGGA
1501 -----+-----+-----+-----+-----+-----+-----+ 1560
AGTGGAGGCCACACAGACGTCGGGCCTGTGATTCCCTCTACCTACTTACCCACCCCTCCT

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TGCGGCGCACATGGCCCCGGGCGGCTCGGCGGTCAGCTGCCGCCCCACAGCGGACCGGT
1561 -----+-----+-----+-----+-----+-----+ 1620
ACGCCGCGTGTAACCGGGGCCCCGCCGAGCCGCCAGTCGACGGCGGGGGTGTGCCTGGCCA

CGGGGCGGGGTCGGGCGGTAGAAAAAAGGGCCGCGAGGCGAGCGGGGCACTGGGCGGAC
1621 -----+-----+-----+-----+-----+-----+ 1680
GCCCCGCCCCCAGCCGCCATCTTTTTCGGCGCTCCGCTCGCCCCGTGACCCGCCTG

CGCGGCGGCAGCATGAGCGGCGCAGACCGTAGCCCCAATGCGGGCGCAGCCCCCTGACTCG
1681 -----+-----+-----+-----+-----+-----+ 1740
GCGCCGCCGTCGTACTCGCCGCGTCTGGCATCGGGGTACGCCCCGCTCGGGGACTGAGC

      M S G A D R S P N A G A A P D S -

GCCCCGGGCCAGGCGGCGGTGGCTTCGGCCTACCAGCGCTTCGAGCCGCGCGCCTACCTC
1741 -----+-----+-----+-----+-----+-----+ 1800
CGGGGCCCCGGTCCGCCGCCACCGAAGCCGGATGGTCGCGAAGCTCGGCGCGCGGATGGAG

A P G Q A A V A S A Y Q R F E P R A Y L -

CGCAACAATAACGCGCCCCCTCGCGGGGACCTGTGCAACCCGAAGGGCGTCGGGCCGTGG
1801 -----+-----+-----+-----+-----+-----+ 1860
GCGTTGTTGATGCGCGGGGGAGCGCCCCTGGACACGTTGGGCTTCCGCGAGCCCGGCACC

R N N Y A P P R G D L C N P N G V G P W -

AAGCTGCGCTGCTTGGCGCAGACCTTCGCCACCGGTGAGCGGGGAAACTGAGGCACGAG
1861 -----+-----+-----+-----+-----+-----+ 1920
TTCGACGCGACGAACCGCGTCTGGAAGCGGTGGCCTACTCGCCCCCTTTGACTCCGTGCTC

K L R C L A Q T F A T G (SEQ ID NO:3)

GGACAAGAGGTCGTCGGGGAGTGAAAGCAGGCGCAGGGAAAATAAAAAAGAAGGAAAGGGAG
1921 -----+-----+-----+-----+-----+-----+ 1980
CCTGTTCTCCAGCAGCCCCCTCACTTTCGTCCGCGTCCCTTTATTTTCTTCCCTTCCCTC

ACAGACCAGGCGCCTAACAGATGGGGACCAAGAAACAAGAGATAGCTGAGAGGTGCAAAC
1981 -----+-----+-----+-----+-----+-----+ 2040
TGTCTGGTCCGCGGATTGTCTACCCCTGGTTCTTGTCTCTATCGACTCTCCACGTTTG

AGAAGAGAAAAAGGAGCAACATCCCTTAGGAGAGGGGCGAGAGGAGAGAGGTGGAGAGA
2041 -----+-----+-----+-----+-----+-----+ 2100
TCTTCTCTTTTTCCTCGTTGTAGGGAATCCTCTCCCCGTCTCCTCTCTCTCCACCTCTCT

GGGGGCGGAGAGTGCTCAGAATTGAGAGCTAAGGTGGGGGATGCAGGACAGACTGAGGTG
2101 -----+-----+-----+-----+-----+-----+ 2160
CCCCGCCTCTCACGAGTCTTAACCTCTCGATTCCACCCCTACGTCTGTCTGACTCCAC

GAGATGCATAGGAGGAAATGGAGGCAGATGTGGGACAGGGGTGAGAACTCCAGGATTTCT
2161 -----+-----+-----+-----+-----+-----+ 2220
CTCTACGTATCCTCCTTTACCTCCGTCTACACCCTGTCCCCACTCTTTGAGGTCCATAAG

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CTCGCTGAGCCTGGCTGGTAGGTATAGTTGTTTCTTTCTTTTCTTTATTTTATTTTCA  
 2221 -----+-----+-----+-----+-----+-----+ 2280  
 GAGCGACTCGGACCGACCATCCATATCAACAAAAGAAAAGAAAAGAAATAAAATAAAAGT  
 TTTATTTACTTATTTTATTTTATTTTATTTTGTGAGACGGAGTTTCGCTCTTGTGCCCCA  
 2281 -----+-----+-----+-----+-----+-----+ 2340  
 AAATAAATGAATAAAAAATAAAAAATAAACAAAACCTCTGCCTCAAAGCGAGAACACGGGT  
 GGCTGGAGTACAATGGCGCCATCTCGGCTCACTGCAACCTCCGCTCCCCGGGTTCAAGC  
 2341 -----+-----+-----+-----+-----+-----+ 2400  
 CCGACCTCATGTTACCGCGGTAGAGCCGAGTGACGTTGGAGGCGGAGGGGCCAAGTTCG  
 GATTCTCTTGCCCTCAGCTTCCCTAGTAGCTGGGATTACAGGCATGCGCCCCCATGCCTGG  
 2401 -----+-----+-----+-----+-----+-----+ 2460  
 CTAAGAGAACGGAGTCGAAGGGATCATCGACCCCTAATGTCCGTACGCGGGGGTACGGACC  
 CTAATTTATTTGTATTTTATTTAGTAGAGACGGGACTTCTCCATGTTGGTCAAGCTGGTCTCG  
 2461 -----+-----+-----+-----+-----+-----+ 2520  
 GATTAAATAAACATAAAAAATCATCTCTGCCTGAAGAGGTACAACCAGTCCGACCAGAGC  
 AACTCCCAACCTTAGGATCCACCCACCCCGGCTCCCAAAGTGCTGGGATTACAGGTGTG  
 2521 -----+-----+-----+-----+-----+-----+ 2580  
 TTGAGGGTTGGAATCCTAGGTGGGTGGGGCCGAGGGTTTCACGACCCTAATGTCCACAC  
 AGCCACTGCGCCCGGCCAGTAGGTATAGTCTTCTAGATGTGAAACCTGAGTCTCAGAGCG  
 2581 -----+-----+-----+-----+-----+-----+ 2640  
 TCGGTGACGCGGGCCGGTCATCCATATCAGAAGATCTACACTTTGGACTCAGAGTCTCGC  
 GTGAAGTTCCGTTCCGAAGGGCAGCCCATGTTGGAGCTGGGTTTCACTCTAACTCTGGGGC  
 2641 -----+-----+-----+-----+-----+-----+ 2700  
 CACTTCAAGGGAAGGCTTCCCGTCGGGTACAACCTCGACCCAAGTCAGATTGAGACCCCG  
 CAATGCTTTTCCAGATGGAGACACATTTGCAGAGGAGAAGGAAGAACTAGAGAGAGGCA  
 2701 -----+-----+-----+-----+-----+-----+ 2760  
 GTTACGAAAAAGGTCTACCTCTGTGTAAACGTCTCCTCTTCTTCTTGATCTCTCTCCGT  
 GGGAGATGCAGGGGAGGGAAGGGTAAGGAGGCAGGGGCTGCCTGGGCTGGCTGGCACCAG  
 2761 -----+-----+-----+-----+-----+-----+ 2820  
 CCCTCTACGTCCCCCTCCCTTCCCATTCCTCCGTCCCCGACGGACCCGACCGACCGTGGTC  
 GACCCCTCTTCTCTGCCCTGCCAGGTGAAGTGTCGGGACGCACCCCTCATCGACATTGGT  
 2821 -----+-----+-----+-----+-----+-----+ 2880  
 CTGGGAGAAGGAGACGGGACGGGTCCACTTCACAGGCCTGCGTGGGAGTAGCTGTAACCA  
 E V S G R T L I D I G -  
 TCAGGCCCCACCGTGTAACAGCTGCTCAGTGCTGCAGCCACTTTGAGGACATGACCATG  
 2881 -----+-----+-----+-----+-----+-----+ 2940  
 AGTCCGGGGTGGCACATGGTTCGACGAGTCACGGACGTCGGTGAAACTCCTGTAGTGGTAC  
 S G P T V Y Q L L S A C S H F E D I T M -

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ACAGATTTCCTGGAGGTCAACCGCCAGGAGCTGGGGGCTGGCTGCAGGAGGAGCCGGGG  
 2941 -----+-----+-----+-----+-----+-----+ 3000  
 TGTCTAAAGGACCTCCAGTTGGCGGTCTCGACCCCGACCGACGTCTCTCGGCCCC  
  
 T D F L E V N R Q E L G R W L Q E E P G -  
  
 GCCTTCAACTGGAGCATGTACAGCCAACATGCCTGCCTCATTGAGGGCAAGGGGTAAGGA  
 3001 -----+-----+-----+-----+-----+-----+ 3060  
 CGGAAGTTGACCTCGTACATGTCGGTTGTACGGACGGAGTAACTCCCGTTCCCCATTCTT  
  
 A F N W S M Y S Q H A C L I E G K G (SEQ ID NO:4)  
  
 CTGGGGGGTGAGGGTTGGGGAGGAGGCTTCCCATAGAGTGGCTGGTTGGGGCAACAGAGG  
 3061 -----+-----+-----+-----+-----+-----+ 3120  
 GACCCCCCACTCCCAACCCCTCCTCCGAAGGGTATCTCACCGACCAACCCCGTTGTCTCC  
  
 CCTGAGCGTAGAACAGCCTTGAGCCCTGCCTTGTGCCTCCTGCACAGGGAATGCTGGCAG  
 3121 -----+-----+-----+-----+-----+-----+ 3180  
 GGACTCGCATCTTGTTCGGAACTCGGGACGGAACACGGAGGACGTGTCCCTTACGACCGTC  
  
  
 E C W Q -  
  
 GATAAGGAGCGCCAGCTGCGAGCCAGGGTGAAACGGGTCCTGCCCATCGACGTGCACCAG  
 3181 -----+-----+-----+-----+-----+-----+ 3240  
 CTATTCTCTCGCGGTTCGACGCTCGGTCCCACTTGCGCCAGGACGGGTAGCTGCACGTGGTC  
  
 D K E R Q L R A R V K R V L P I D V H Q -  
  
 CCCCAGCCCCTGGGTGCTGGGAGCCCAGCTCCCCTGCCTGCTGACGCCCTGGTCTCTGCC  
 3241 -----+-----+-----+-----+-----+-----+ 3300  
 GGGGTCTGGGGACCCACGACCTCTGGGTCTGAGGGGACGGACGACTGCGGGACCAGAGACGG  
  
 P Q P L G A G S P A P L P A D A L V S A -  
  
 TTCTGCTTGGAGGCTGTGAGCCCAGATCTTGCCAGCTTTTACGCGGGCCCTGGACCACATC  
 3301 -----+-----+-----+-----+-----+-----+ 3360  
 AAGACGAACCTCCGACACTCGGGTCTAGAACGGTCGAAAGTCGCCCCGGGACCTGGTGTAG  
  
 F C L E A V S P D L A S F Q R A L D H I -  
  
 ACCACGCTGCTGAGGCCTGGGGGGCACCTCCTCCTCATCGGGGGCCCTGGAGGAGTCGTGG  
 3361 -----+-----+-----+-----+-----+-----+ 3420  
 TGGTGCAGGACTCCGGACCCCCCTGGAGGAGGAGTAGCCCCGGGACCTCCTCAGCACC  
  
 T T L L R P G G H L L L I G A L E E S W -  
  
 TACCTGGCTGGGGAGGCCAGGCTGACGGTGGTGCCAGTGTCTGAGGAGGAGGTGAGGGAG  
 3421 -----+-----+-----+-----+-----+-----+ 3480  
 ATGGACCGACCCCTCCGGTCCGACTGCCACCACGGTCACAGACTCCTCCTCCACTCCCTC  
  
 Y L A G E A R L T V V P V S E E E V R E -

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```
GCCCTGGTGCGTAGTGGCTACAAGGTCCGGGACCTCCGCACCTATATCATGCCTGCCCAC
3481 -----+-----+-----+-----+-----+-----+ 3540
CGGGACCACGCATCACCGATGTTCCAGGCCCTGGAGGCGTGGATATAGTACGGACGGGTG

A L V R S G Y K V R D L R T Y I M P A H -

CTTCAGACAGGCGTAGATGATGTCAAGGGCGTCTTCTTCGCCTGGGCTCAGAAGGTTGGG
3541 -----+-----+-----+-----+-----+-----+ 3600
GAAGTCTGTCCGCATCTACTACAGTTCCTCGCAGAAGAAGCGGACCCGAGTCTTCCAACCC

L Q T G V D D V K G V F F A W A Q K V G -

CTGTGAGGGCTGTACCTGGTGCCCTGTGGCCCCCACCACCTGGATTCCCTGTTCTTTGA
3601 -----+-----+-----+-----+-----+-----+ 3660
GACACTCCCGACATGGACCACGGGACACCGGGGGTGGGTGGACCTAAGGGACAAGAACT

L * (SEQ ID NO:5)

AGTGGCACCTAATAAAGAAATAATACCCTGCCGCTGCGGTCAGTGCTGTGTGTGGCTCTC
3661 -----+-----+-----+-----+-----+-----+ 3720
TCACCGTGGATTATTTCTTTATTATGGGACCGCGACGCCAGTCACGACACACACCGAGAG

CTGGGAAGCAGCAAGGGCCCAGAGATCTGAGTGTCCGGGTAGGGGAGACATTACCCCTAG
3721 -----+-----+-----+-----+-----+-----+ 3780
GACCCCTTCGTCGTTCCCGGGTCTCTAGACTCACAGGCCCATCCCTCTGTAAGTGGGATC

GCTTTTTTTTCCAGAAGCTT (SEQ ID NO:1)
3781 -----+----- 3799
CGAAAAAAAGGTCTTCGAA (SEQ ID NO:2)
```

Figure 2A – page 1

```

GGCAGCATGAGCGGCGCAGACCGTAGCCCCAATGCGGGCGCAGCCCCTGACTCGGCCCCG
1  -----+-----+-----+-----+-----+-----+ 60
CCGTCGTACTCGCCGCGTCTGGCATCGGGGTACGCCCCGCGTCGGGACTGAGCCGGGGC

      M S G A D R S P N A G A A P D S A P -

GGCCAGGCGGCGGTGGCTTCGGCCTACCAGCGCTTCGAGCCGCGCGCCTACCTCCGCAAC
61 -----+-----+-----+-----+-----+-----+ 120
CCGGTCCGCCGCCACCGAAGCCGGATGGTCGCGAAGCTCGGCGCGCGGATGGAGGCGTTG

      G Q A A V A S A Y Q R F E P R A Y L R N -

AACTACGCGCCCCCTCGCGGGGACCTGTGCAACCCGAACCGGCGTCGGGCCGTGGAAGCTG
121 -----+-----+-----+-----+-----+-----+ 180
TTGATGCGCGGGGAGCGCCCCCTGGACACGTTGGGCTTGCCGCAGCCCGGCACCTTCGAC

      N Y A P P R G D L C N P N G V G P W K L -

CGCTGCTTGGCGCAGACCTTCGCCACCGGTGAAGTGTCGGACGCACCCTCATCGACATT
181 -----+-----+-----+-----+-----+-----+ 240
GCGACGAACCGCGTCTGGAAGCGGTGGCCACTTCACAGGCCTGCGTGGGAGTAGCTGTAA

      R C L A Q T F A T G E V S G R T L I D I -

GGTTCAGGCCCCACCGTGTACCAGCTGCTCAGTGCCTGCAGCCACTTTGAGGACATCACC
241 -----+-----+-----+-----+-----+-----+ 300
CCAAGTCCGGGGTGGCACATGGTCGACGAGTCACGGACGTCGGTGAAACTCCTGTAGTGG

      G S G P T V Y Q L L S A C S H F E D I T -

ATGACAGATTTCTGAGGTCAACCGCCAGGAGCTGGGGCGCTGGCTGCAGGAGGAGCCG
301 -----+-----+-----+-----+-----+-----+ 360
TACTGTCTAAAGGACCTCCAGTTGGCGGTCTCGACCCCSCGACCGACGTCCTCCTCGGC

      M T D F L E V N R Q E L G R W L Q E E P -

GGGGCCTTCAACTGGAGCATGTACAGCCAACATGCCTGCCTCATTGAGGGCAAGGGGGAA
361 -----+-----+-----+-----+-----+-----+ 420
CCCCGGAAGTTGACCTCGTACATGTCGGTTGTACGGACGGAGTAACTCCCGTTCCCCCTT

      G A F N W S M Y S Q H A C L I E G K G E -

TGCTGGCAGGATAAGGAGCGCCAGCTGCGAGCCAGGGTGAAACGGGTCTGCCCATCGAC
421 -----+-----+-----+-----+-----+-----+ 480
ACGACCGTCCTATTCTCGCGGTGACGCTCGGTCCCACTTTGCCCAGGACGGGTAGCTG

      C W Q D K E R Q L R A R V K R V L P I D -

GTGCACCAGCCCCAGCCCCCTGGGTGCTGGGAGCCCAGCTCCCCTGCCTGCTGACGCCCTG
481 -----+-----+-----+-----+-----+-----+ 540
CACGTGGTTCGGGGTCGGGGACCCACGACCCTCGGGTCGAGGGGACGGACGACTGCGGGAC

      V H Q P Q P L G A G S P A P L P A D A L -

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**Figure 2A – page 2**

```
GTCTCTGCCTTCTGCTTGGAGGCTGTGAGCCCAGATCTTGCCAGCTTTCAGCGGGCCCTG
541 -----+-----+-----+-----+-----+-----+ 600
CAGAGACGGAAGACGAACCTCCGACACTCGGGTCTAGAACGGTCGAAAGTCGCCCCGGGAC

V S A F C L E A V S P D L A S F Q R A L -

GACCACATCACCACGCTGCTGAGGCCTGGGGGGCACCTCCTCCTCATCGGGGCCCTGGAG
601 -----+-----+-----+-----+-----+-----+ 660
CTGGTGTAGTGGTGCACGACTCCGACCCCCCGTGGAGGAGGAGTAGCCCCGGGACCTC

D H I T T L L R P G G H L L L I G A L E -

GAGTCGTGGTACCTGGCTGGGGAGGCCAGGCTGACGGTGGTGCCAGTGTCTGAGGAGGAG
661 -----+-----+-----+-----+-----+-----+ 720
CTCAGCACCATGGACCGACCCCTCCGGTCCGACTGCCACCACGGTCACAGACTCCTCCTC

E S W Y L A G E A R L T V V P V S E E E -

GTGAGGGAGGCCCTGGTGCCTAGTGGCTACAAGGTCCGGGACCTCCGCACCTATATCATG
721 -----+-----+-----+-----+-----+-----+ 780
CACTCCCTCCGGGACCACGCATCACCGATGTTCCAGGCCCTGGAGGCGTGGATATAGTAC

V R E A L V R S G Y K V R D L R T Y I M -

CCTGCCCACCTTCAGACAGGCGTAGATGATGTCAAGGGCGTCTTCTTCGCCTGGGCTCAG
781 -----+-----+-----+-----+-----+-----+ 840
GGACGGGTGGAAGTCTGTCCGCATCTACTACAGTTCCCGCAGAAGAAGCGGACCCGAGTC

P A H L Q T G V D D V K G V F F A W A Q -

AAGGTTGGGCTGTGAGGGCTGTACCTGGTGGCCCTGTGGCCCCCACCACCTGGATTCCCT
841 -----+-----+-----+-----+-----+-----+ 900
TTCCAACCCGACACTCCCGACATGGACCACGGGACACCGGGGGTGGGTGGACCTAAGGGA

K V G L * (SEQ ID NO:8)

GTTCTTTGAAGTGGCACCTAATAAAGAAATAATACC (SEQ ID NO:6)
901 -----+-----+-----+-----+-----+ 936
CAAGAACTTCACCGTGGATTATTTCTTTATTATGG (SEQ ID NO:7)
```



**Figure 2B**

```
MSGADRSPNAGAAPDSAPGQAAVASAYQRFEPRAYLRNNYAPPRGDLCPNGVGPWKLRC
1  -----+-----+-----+-----+-----+-----+ 60

LAQTFATGEVSGRTLIDIGSGPTVYQLLSACSHFEDITMTDFLEVNRQELGRWLQEEPGA
61  -----+-----+-----+-----+-----+-----+ 120

FNWSMYSQHACLIEGKGECWQDKERQLRARVKRVLPIDVHQPPPLGAGSPAPLPADALVS
121 -----+-----+-----+-----+-----+-----+ 180

AFCLEAVSPDLASFQRALDHITLLRPGGHLLLIGALEESWYLAGEARLTVVPVSEEEVR
181 -----+-----+-----+-----+-----+-----+ 240

EALVRSGYKVRDLRTYIMPAHLQTVDDVKGVFFAWAQKVGL (SEQ ID NO:8)
241 -----+-----+-----+-----+-----+--- 282
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**Figure 3**